AMENDMENTS TO THE SPECIFICATION:

Please amend the specification as follows:

Please delete the paragraph spanning lines 21-33 of page 3 and insert the following therefor:

Methods for the search and identification of TAD homologues would be well within the realm of persons skilled in the art. Such methods comprise comparison of the sequences represented by SEQ ID NO 1 or 2 in a computer readable format with sequences that are available in public databases such as MIPS (URL mips.gsf.de ~~http://mips.gsf.de/~~), GenBank (URL ncbi.nlm.nih.gov/Genbank/index ~~http://www.ncbi.nlm.nih.gov/Genbank/index.html~~) or EMBL Nucleotide Sequence Database (URL ebi.ac.uk/embl/index ~~http://www.ebi.ac.uk/embl/index.html~~), using algorithms well known in the art for alignment or comparison of sequences, such as GAP (Needleman and Wunsch, J. Mol. Biol. 48, 443-453 (1970)), BESTFIT (using the local homology algorithm of Smith and Waterman (Advances in Applied Mathematics 2, 482-489 (1981))), BLAST (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J., J. Mol. Biol. 215, 403-410 (1990)), FASTA and TFASTA (W. R. Pearson and D. J. Lipman, Proc. Natl. Acad. Sci. USA 85, 2444-2448 (1988)). The software for performing BLAST analysis is publicly available at the National Centre for Biotechnology Information.

Please delete the paragraph spanning lines 1-20 of page 4 and insert the following therefor:

These above-mentioned analyses for sequence homology can be done with a full-length query sequence or with certain regions of such a sequence, for example with conserved domains. Also the identification of family members of the TAD (as defined below) or the determination of the percentage of sequence identity between the TAD and a homologue (as defined below) can be performed by using these conserved sequences. The identification of such domains in a protein sequence would also be well within the realm of the person skilled in the art and involve a computer readable format of the nucleic acids used in the present invention, the use of alignment software programs and the use of publicly available information on protein domains, conserved motifs and boxes. An integrated search can be done using the INTERPRO database (Mulder et al., (2003) Nucl. Acids Res. 31, 315-318, http://www.ebi.ac.uk/interpro/scan.html) which combines several databases on protein families, domains and functional sites, such as the PRODOM (Servant et al., (2002) Briefings in Bioinformatics 3, 246-251, http://prodes.toulouse.inra.fr/prodom/2002.1/html/home.php), PIR (Huang et al. (2003) Nucl. Acids Res. 31, 390-392, http://pir.georgetown.edu/) or Pfam (Bateman et al. (2002) Nucl. Acids Res. 30, 276-280, URL pfam.wustl.edu ~~http://pfam.wustl.edu/~~) databases. Sequence analysis programs designed for motif searching can be used for identification of conserved fragments, regions and domains as mentioned above. Suitable computer programs to this end include for example MEME (Bailey and Elkan

(1994) Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology, pp. 28-36, AAAI Press, Menlo Park, California, http://meme.sdsc.edu/meme/website/intro.html).

Please delete the paragraph spanning lines 14-30 of page 5 and insert the following therefor:

Two special forms of homology, orthologous and paralogous homology, are evolutionary concepts used to describe ancestral relationships of genes. The term "paralogous" relates to homologous genes that result from one or more gene duplications within the genome of a species. The term "orthologous" relates to homologous genes in different organisms due to ancestral relationship of these genes. The term "homologues" as used herein also encompasses paralogues and orthologues of the proteins useful in the methods according to the invention. Orthologous genes can be identified by querying one or more gene databases with a query gene of interest, using for example the BLAST program. The highest-ranking subject genes that result from the search are then again subjected to a BLAST analysis, and only those subject genes that match again with the query gene are retained as true orthologous genes. For example, to find a rice orthologue of an *Arabidopsis thaliana* gene, one may perform a BLASTN or TBLASTX analysis on a rice database (such as (but not limited to) the *Oryza sativa* Nipponbare database available at the NCBI (URL ncbi.nlm.nih.gov ~~http://www.ncbi.nlm.nih.gov~~) or the genomic sequences of rice (cultivars indica or japonica)). In a next step, the obtained rice sequences are used in a reverse BLAST analysis using an *Arabidopsis* database. The results may be further refined when the

resulting sequences are analysed with ClustalW and visualised in a neighbour joining tree. The method can be used to identify orthologues from many different species.

Please delete the paragraph spanning lines 10-14 of page 26 and insert the following therefor:

Figure 1: Schematic presentation of the entry clone p69, containing CDS0671 within the AttL1 and AttL2 sites for GATEWAY[[Gateway®]]-cloning (bacteriophage lambda site specific recombinant cloning) in the pDONR201 backbone. CDS0671 is the internal code for the TOB3-like AAA-ATPase domain coding sequence of *Nicotiana tabacum* BY2 cells. This vector contains also a bacterial kanamycine-resistance cassette and a bacterial origin of replication.

Please delete the paragraph spanning page 28, from line 28 through line 8 of page 29 and insert the following therefor:

A cDNA library with an average size of inserts of 1,400 bp was prepared from poly(A^+) RNA isolated from actively dividing, non-synchronized BY2 tobacco cells. These library-inserts were cloned in the vector pCMVSPORT6.0, comprising an attB GATEWAY [[Gateway]] cassette (an attB recombinant cassette -Life Technologies). From this library, 46,000 clones were selected, arrayed in 384-well microtiter plates, and subsequently spotted in duplicate on nylon filters. The arrayed clones were screened using pools of several hundreds of radioactively labelled tags as probe (including the BY2-tag corresponding to the sequence CDS0671, SEQ IDNO 1). Positive clones were

isolated (among which was the clone corresponding to CDS0671, SEQ ID NO 1), sequenced, and aligned with the tag sequence. In cases where hybridisation with the tag failed, the full-length cDNA corresponding to the tag was selected by PCR amplification: tag-specific primers were designed using primer3 program (URL genome.wi.mit.edu/genome_software/other/primer3 ~~http://www-genome.wi.mit.edu/genome_software/other/primer3.html~~) and used in combination with a common vector primer to amplify partial cDNA inserts. Pools of DNA from 50,000, 100,000, 150,000, and 300,000 cDNA clones were used as templates in the PCR amplifications. Amplification products were then isolated from agarose gels, cloned, sequenced and their sequence aligned with those of the tags.

Please delete the paragraph spanning lines 9-11 of page 29 and insert the following therefor:

Next, the full-length cDNA corresponding to the nucleotide sequence of SEQ ID NO 1 was cloned from the pCMVsport6.0 library vector into pDONR201, a GATEWAY [[Gateway®]] donor vector (a donor vector - Invitrogen, Paisley, UK) via a LR reaction, resulting in the entry clone p69 (Figure 1).

Please delete the paragraph spanning lines 14-18 of page 29 and insert the following therefor:

The entry clone p69 was subsequently used in an LR reaction with p0830, a destination vector used for *Oryza sativa* transformation. This vector contains as

functional elements within the T-DNA borders: a plant selectable marker; a screenable marker; and a [[Gateway]]GATEWAY cassette (recombinant cassette) intended for LR in vivo recombination with the sequence of interest already cloned in the entry clone. Promoter PRO0090 was located upstream of this [[Gateway]]GATEWAY cassette.